Precursor and temperature modulation of fatty acid composition and growth of *Listeria* monocytogenes cold-sensitive mutants with transposon-interrupted branched-chain α -keto acid dehydrogenase

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Branched-chain fatty acids (BCFAs) typically constitute more than 90 % of the fatty acids of Listeria monocytogenes. The authors have previously described two Tn917-induced, cold-sensitive, BCFA-deficient (<40%) L. monocytogenes mutants (cld-1 and cld-2) with lowered membrane fluidity. Sequence analyses revealed that Tn917 was inserted into different genes of the branched-chain α -keto acid dehydrogenase cluster (bkd) in these two mutants. The cold-sensitivity and BCFA deficiency of cld-1, in which Tn917 was inserted into bkdB, were complemented in trans by cloned bkdB. The growth and corresponding BCFA content of the mutants at 37 °C were stimulated by fatty acid precursors bypassing Bkd, 2-methylbutyrate (precursor for odd-numbered anteiso-fatty acids), isobutyrate (precursor for even-numbered iso-fatty acids) and isovalerate (precursor for odd-numbered iso-fatty acids). In contrast, the corresponding Bkd substrates, α -ketomethylvalerate, α -ketoisovalerate and α -ketoisocaproate, exhibited much poorer activity. At 26 °C, 2-methylbutyrate and isovalerate stimulated the growth of the mutants, and at 10 °C, only 2-methylbutyrate stimulated growth. Pyruvate depressed the BCFA content of cld-2 from 33 % to 27 %, which may be close to the minimum BCFA requirement for L. monocytogenes. The transcription of bkd was enhanced by Bkd substrates, but not by low temperature. When provided with the BCFA precursors, cld-2 was able to increase its anteiso-C_{15:0} fatty acid content at 10 °C compared to 37 °C, which is the characteristic response of L. monocytogenes to low temperature. This implies that Bkd is not the major cold-regulation point of BCFA synthesis.

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INTRODUCTION

Listeria monocytogenes causes the potentially life-threatening infection known as listeriosis, which has a fatality rate of 20–25 % (Mead *et al.*, 1999). Listeriosis outbreaks have been linked to the consumption of food contaminated with this organism. Nowadays, there is an increased consumption of ready-to-eat, chilled and frozen foods, with decreased use of chemical microbial control agents. The ability of

Abbreviations: BCFA, branched-chain fatty acid; Bkd, branched-chain α -keto acid dehydrogenase; IB, isobutyrate; IV, isovalerate; KIC, α -ketoisocaproate; KIV, α -ketoisovalerate; KMV, α -ketomethylvalerate; MB, 2-methylbutyrate; PDH, pyruvate dehydrogenase.

The GenBank accession number for the sequence reported in this paper is AY138856.

L. monocytogenes to grow at refrigeration temperatures is a critical aspect of its role as a food-borne pathogen, since refrigeration temperature inhibits the growth of most other food-borne pathogens (Bryan, 2004). However, the underlying psychrotolerance mechanism is not completely understood, and a better understanding may result in a novel strategy for controlling the growth of L. monocytogenes at low temperatures.

Low temperature has profound effects on all aspects of microbial cell structure and function, involving the structural integrity of macromolecules, macromolecular assemblies, protein synthesis and nutrient uptake (Panoff *et al.*, 1998; Weber & Marahiel, 2002). Small, nucleic-acid-binding, cold-shock proteins play key roles in resuming growth under cold shock (Panoff *et al.*, 1998). Low

temperature also reduces membrane fluidity, and causes membrane phase transitions from a liquid-crystalline state to a more rigid gel-like state. To restore membrane functionality at low temperatures, fatty acids with low melting points are incorporated into lipids. The two most common ways bacteria increase membrane fluidity are by incorporating unsaturated and branched-chain fatty acids (BCFAs), which have lower melting points than the corresponding saturated straight-chain fatty acids, into their lipids (Suutari & Laakso, 1994). The L. monocytogenes membrane-fatty-acid composition is dominated to an unusual extent by BCFAs (>90% of the total fatty acid content) (Annous et al., 1997). Among the common BCFAs in L. monocytogenes, anteiso-C_{15:0} has the lowest melting point (Kaneda, 1991). When the growth temperature declines, anteiso- $C_{15:0}$ content in the membrane rises to maintain optimal membrane fluidity (Annous et al., 1997; Edgcomb et al., 2000; Nichols et al., 2002).

Two Tn917 transposon-induced mutants (*cld-1* and *cld-2*) have lost the ability to grow at 4 °C on solid media, but are not defective in the induction of cold-shock proteins (Bayles *et al.*, 1996). These mutants are deficient in the production of odd-numbered BCFAs, and exhibit atypical amounts of even-numbered straight-chain and iso-BCFAs (Annous *et al.*, 1997; Edgcomb *et al.*, 2000). The membranes

of strain cld-1 are significantly less fluid than those of the parent strain (Edgcomb et al., 2000; Jones et al., 2002). To further characterize this mechanism of psychrotolerance, it was important to identify the disrupted gene(s) that caused the cold-sensitive phenotype in the mutants. Based on the observations above, we speculated that the insertion of Tn917 into cld-1 and cld-2 may interrupt the gene(s) involved in BCFA biosynthesis (Annous et al., 1997). In bacteria, the branched-chain portion of fatty acids derives primarily from the branched-chain amino acids (Kaneda, 1991; de Mendoza et al., 2002). Moreover, incorporation of a methyl branch can only be achieved by de novo biosynthesis of fatty acid (Suutari & Laakso, 1994). Previous studies of BCFA biosynthesis have primarily focused on Bacillus subtilis (de Mendoza et al., 2002). Two critical enzymes in the pathway from branched-chain amino acids to BCFA have been reported: branched-chain α-keto acid dehydrogenase (Bkd) and β -ketoacyl-acyl carrier protein synthase III (FabH) (Oku & Kaneda, 1988; Choi et al., 2000; Lu et al., 2004). Isoleucine, valine and leucine are transaminated by branched-chain amino acid transaminase, and are subsequently oxidatively decarboxylated by the Bkd complex, resulting in production of the short branchedchain acyl-CoA derivatives 2-methylbutyryl-CoA, isobutyryl-CoA and isovaleryl-CoA (Fig. 1). These acyl-CoA precursors are then utilized by FabH as starting units to initiate BCFA

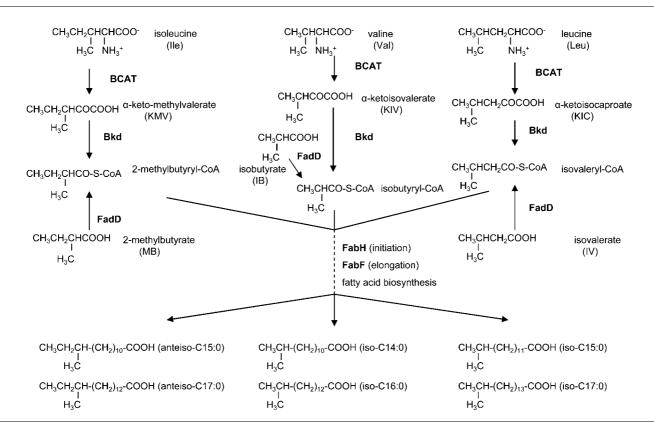


Fig. 1. Schematic biosynthesis pathway of starting units for BCFAs from branched-chain amino acids in *L. monocytogenes*. BCAT, branched-chain amino acid transaminase; Bkd, branched-chain α -keto acid dehydrogenase; FabH, β -ketoacyl-ACP synthase III; FadD, acyl-CoA synthetase; FabF, β -ketoacyl ACP synthase II.

biosynthesis (Fig. 1). Although the cold-regulated fatty acid adjustment is one universal adaptation to low temperature, the underlying mechanism of cold-regulated BCFA synthesis is not well characterized (de Mendoza *et al.*, 2002; Lu *et al.*, 2004) Here, we identified that the two *L. monocytogenes* cold-sensitive mutants (*cld-1* and *cld-2*) had Tn917 inserted into the *bkd* cluster. We also attempted to determine the role of Bkd in biosynthesis and cold-regulation of BCFA.

METHODS

Bacterial strains and growth conditions. L. monocytogenes parent strain 10403S, and transposon-insertion mutants cld-1 and cld-2, were used in this study (Annous et al., 1997; Bayles et al., 1996). These strains were grown in BHI (Difco) supplemented with erythromycin (1 $\mu g \ ml^{-1}$) and lincomycin (25 $\mu g \ ml^{-1}$) for strains cld-1 and cld-2, at 37 °C with shaking (150 r.p.m.), unless specified otherwise. Escherichia coli strain Top10 (Invitrogen) was grown in Luria-Bertani (LB) medium at 37 °C with shaking (220 r.p.m.). When necessary, ampicillin, kanamycin and tetracycline were added to final concentrations of 100, 20 and 10 µg ml⁻¹, respectively. For preparation of L. monocytogenes cultures for growth studies and fatty acid analysis, the 5 ml starter culture without supplements was prepared as described above. For all strains, a 2 ml volume of the overnight starter culture was used to inoculate 100 ml BHI medium without antibiotics in a 250 ml Erlenmeyer flask. All supplements, short BCFAs, branched-chain α-keto acids and pyruvate were added to the medium as filter-sterilized solutions. Growth was monitored by measuring OD_{600} using a Beckman DU-65 spectrophotometer.

Molecular biological methods. Unless specified, all molecular biological methods were performed as described by Sambrook *et al.* (1989). Chromosomal DNA from *L. monocytogenes* was isolated using a Wizard Genomic DNA Purification Kit (Promega) according to the manufacturer's manual, except that cells were lysed by lysozyme (20 μ g ml⁻¹) at 37 °C for 60 min.

Cloning and sequencing the L. monocytogenes DNA adjacent to the transposon insertions. The L. monocytogenes mutants in this study carry a Tn917 insertion (Camilli et al., 1990). Genomic DNA was digested with restriction enzyme EcoRI, self-ligated and transformed into E. coli Top10 (Invitrogen). Plasmid DNA was isolated from kanamycin-resistant transformants using a miniprep kit (Qiagen). Chromosomal DNA in the resultant plasmid was sequenced using the Dye Terminator Cycle Sequencing Kit and an ABI Prism 310 sequencer (Applied Biosystems). The sequencing reaction was performed using two oligonucleotides 5'-GGAGCATATCACTTTT-CTTGGAGAG-3' and 5'-ACGGTTGAAAACTGTACC-3', respectively corresponding to the 5' and 3' ends of Tn917. Using oligonuleotides 5'-AGATGTTGGGAAAAAAGGTGGC-3' and 5'-CTTGAAGAATA-GCGGCTTGTGG-3', the DNA region that spanned the portion of the genome between the two Tn917 insertion sites was cloned into the PCR cloning vector pCR2.1 (Invitrogen), and subsequently sequenced using primer walking (Fig. 2). The inverse PCR procedure with oligonuleotides 5'-GAAACAATGCTAATGGCGAG and 5'-CTCCAATCGCATAGATGTG-3' was used to amplify the DNA segment beyond the EcoRI site flanking the Tn917 insertion site. Nucleic acid and deduced amino acid sequence data were analysed using MacVector 6.5 edition (Oxford Molecular) and the National Center for Biotechnology Information (NCBI) BLAST network service.

Complementation of mutant *cld-1* **with intact** *bkdB.* The wild-type *bkdB* gene was amplified using primers pE25 (5'-AAA-GGATCCATGCCCAAATTAGGGGAA-3') and pE23 (5'-GAGGA-GTTTTCTTCCGCAATGA-3'). The putative promoter region of the

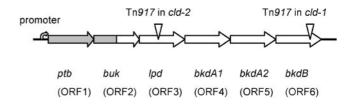


Fig. 2. Molecular organization of the *L. monocytogenes bkd* gene cluster and transposon insertion sites. The DNA sequence of the grey portion was from the *L. monocytogenes* genome sequence (Glaser *et al.*, 2001).

bkd cluster was amplified using primers pMO52 (5'-CACCAAGG-TATTACATCAATTA-3') and pMO32 (5'-TTCGGATCCATCTGA-AAAAAATCTGCTT-3') (Glaser et al., 2001) (Fig. 2). The two fragments were cloned into HindIII and PstI double-digested pKSV7 (Smith & Youngman, 1992), giving rise to pME2K8. The BamHI restriction sites in primer pMO32 and pE25 were used to fuse the promoter region with bkdB into a correct reading frame. A tetracycline resistance gene was subsequently cloned into the HindIII site of pME2K8 to generate pME2K8tet. The electroporation was performed essentially according to the method of Park & Stewart (1990). The transformants were plated on BHI agar containing tetracycline, and incubated at 30 °C for 2–3 days.

RNA isolation and Northern blot analysis. In the branched-chain α -keto acid induction analysis, strain 10403S was grown in BHI medium supplemented with 500 μ M α -ketomethylvalerate at 37 °C. In the cold-induction analysis, strain 10403S was grown in separate BHI cultures at 37 °C and 10 °C. When the OD₆₀₀ reached 0·3–0·4, cells were chilled on ice, and harvested by centrifugation. RNA protection solution (Qiagen) was added to stabilize RNA immediately after harvesting. A 1 ml volume of RLT buffer (RNeasy Mini Kit, Qiagen) and 0·5 g glass beads were added to the cell pellet obtained from 2·5 ml of culture. A bead beater (Biospec Products) was used to break the cells (5000 r.p.m., 20 s, six times). Total RNA was isolated using an RNeasy Mini Kit according to the manufacturer's instructions. RNA was treated with DNase I (Invitrogen) prior to Northern blot analysis. Northern hybridization was performed using the NorthernMax kit according to the manufacturer's manual (Ambion).

Fatty acid analysis. Cultures of *L. monocytogenes* were grown in 100 ml BHI medium at designated temperatures in the presence or absence of the following supplements: short BCFAs bypassing Bkd [2-methylbutyrate (MB), isobutyrate (IB) and isovalerate (IV)], substrates of Bkd [α-ketomethylvalerate (KMV), α-ketoisovalerate (KIV) and α-ketoisocaproate (KIC)] and pyruvate. Cells were harvested in the mid-exponential phase (OD₆₀₀, 0·5–0·7), and the pellet was washed three times with distilled water. The fatty acids in the cells (30–40 mg wet weight) were saponified, methylated and extracted. The resulting methyl ester mixtures were separated by an Agilent 5890 dual-tower gas chromatograph. Fatty acids were identified by the MIDI microbial identification system (Sherlock 4.5 microbial identification system). This analysis was performed at Microbial ID (Newark, DE, USA).

RESULTS

Tn917 was inserted in the bkd region in cld-1 and cld-2

BLAST search of the sequences flanking transposon insertion sites revealed that in *cld-1* and *cld-2*, the transposon

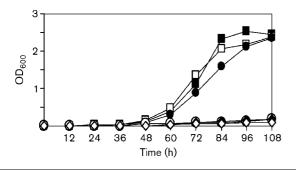


Fig. 3. Growth of *L. monocytogenes* 10403S, *cld-1*, *cld-2*, and their *bkdB*-complemented strains in BHI at 10 °C. \Box , 10403S; ■, 10403S-*bkdB*; \bigcirc , *cld-1*; •, *cld-1-bkdB*; \diamondsuit , *cld-2*; •, *cld-2-bkd*.

appeared to insert in the same gene cluster encoding the Bkd complex. In B. subtilis, which is a close relative of L. monocytogenes, Bkd is a multi-enzyme complex encoded by four genes (Wang et al., 1993); therefore a genome segment of 5600 bp flanking the insertion sites was cloned and sequenced in order to further characterize the bkd cluster. Four complete ORFs (ORF3, 4, 5 and 6) and one incomplete ORF (ORF2) were found in this segment (Fig. 2), all with the same transcription orientation. Deduced amino acid sequences of the four complete ORFs were most similar (35-82% identity) to the subunits of the prokaryotic Bkd complex, including those from B. subtilis and Staphylococcus aureus. ORF3 (lpd), ORF4 (bkdA1), ORF5 (bkdA2) and ORF6 (bkdB) respectively encoded dihydrolipoamide dehydrogenase (E3), decarboxylase $(E1\alpha)$, decarboxylase $(E1\beta)$ and dihydrolipoamide acyltransferase (E2) subunits of the Bkd complex. Specifically, Tn917 was located near the 3' end of bkdB in strain cld-1, and in the middle of lpd in strain cld-2 (Fig. 2). The organization of these genes was identical to the order in B. subtilis and Enterococcus faecalis (Debarbouille et al., 1999; Ward et al., 1999). In addition, a comparison of several L. monocytogenes genomic sequences revealed a BCFA kinase gene (buk, ORF2) and a branched-chain phosphotransacylase gene (ptb, ORF1) upstream of lpd (Fig. 2) (Glaser *et al.*, 2001; Nelson *et al.*, 2004), which were also present in the *bkd* operon of *B. subtilis* and *E. faecalis* (Debarbouille *et al.*, 1999; Ward *et al.*, 1999).

Genetic complementation restores the growth of cld-1 and its BCFA content

In order to confirm that the transposon insertion in the mutants was the cause of the cold-sensitive and BCFAdeficient phenotype, the mutation was complemented by a plasmid bearing the wild-type bkdB gene. Shuttle vector pME2K8tet contained the putative promoter region and the complete bkdB gene (Fig. 2). Transformant cld-1-bkdB grew normally on BHI agar at 37 °C, as did strain 10403S. Furthermore, *cld-1-bkdB* showed the same growth pattern as 10403S at 10 °C (Fig. 3). As shown in Table 1, functional bkdB also restored the normal BCFA content in cld-1 from 39 % to 98 % of total fatty acids. Clearly the BCFAs were closely associated with the growth ability of L. monocytogenes at low temperature. These data demonstrate that bkdB is important for the BCFA synthesis, and that the interrupted bkdB in strain cld-1causes the BCFA deficiency. As a negative control, the intact bkdB did not fully restore the BCFA and growth of cld-2, presumably because of a lack of a wild-type *lpd* gene in the pME2K8tet construct.

BCFA precursors bypassing Bkd stimulate the growth and BCFA content of cld-1 and cld-2

Strains *cld-1* and *cld-2* grew very poorly at 10 °C, and they grew more slowly than parent strain 10403S at 37 °C (Fig. 4). It was expected that BCFA precursors bypassing Bkd, i.e. the short BCFAs MB, IB and IV, would restore the growth and BCFAs of the *bkd* mutants if the primary role of Bkd in *L. monocytogenes* is to produce BCFA precursors (Fig. 1). We previously reported that MB stimulated the growth of *cld-1* and *cld-2* (Annous *et al.*, 1997), and in this study we found that IB and IV could also stimulate the growth of these strains at 37 °C (Fig. 4a). Here and subsequently, growth and fatty acid data are shown for *cld-2* only. The growth of *cld-2* was more impaired, and the BCFA

Table 1. Fatty acid composition of 10403S, cld-1, cld-2 and their bkdB-complemented strains in BHI at 37 °C

The values are the means of at least two independent experiments \pm SEM; some minor fatty acid components are not shown. ND, Not detected.

Strain	Percentage (w/w) of total fatty acids									
	C _{14:0}	Iso-C _{14:0}	C _{15:0}	Iso-C _{15:0}	Anteiso-C _{15:0}	$C_{16:0}$	Iso-C _{16:0}	Iso-C _{16:0}	Anteiso-C _{17:0}	BCFA
10403S	ND	0.7 ± 0.1	ND	10.4 ± 0.4	46.2 ± 0.6	0.9 ± 0.1	2.5 ± 0.1	3.4 ± 0.2	35.3 ± 0.4	98.7
10403S- <i>bkdB</i>	ND	0.7 ± 0.0	ND	10.5 ± 0.3	46.2 ± 0.2	$1 \cdot 2 \pm 0 \cdot 2$	$2 \cdot 6 \pm 0 \cdot 0$	3.5 ± 0.1	35.0 ± 0.3	98.5
cld-1	$18\!\cdot\!1 \pm 1\!\cdot\!1$	10.7 ± 2	6.2 ± 1.6	$2 \cdot 0 \pm 0 \cdot 7$	10.3 ± 1.4	$34 \cdot 2 \pm 1 \cdot 3$	13.3 ± 1.9	ND	3.5 ± 1.5	39.8
cld-1-bkdB	ND	0.5 ± 0.0	ND	$10{\cdot}1 \pm 0{\cdot}4$	47.0 ± 0.4	0.9 ± 0.1	$2 \cdot 2 \pm 0 \cdot 1$	$3 \cdot 4 \pm 0 \cdot 1$	35.6 ± 0.2	98.9
cld-2	$27 \cdot 5 \pm 0 \cdot 7$	13.6 ± 1.6	$5 \cdot 2 \pm 0 \cdot 6$	$1\!\cdot\!0\pm0\!\cdot\!1$	$3 \cdot 1 \pm 0 \cdot 3$	30.8 ± 1.4	14.8 ± 1.5	ND	0.9 ± 0.0	33.6
cld-2-bkdB	17.5 ± 0.8	$16 \cdot 0 \pm 4 \cdot 4$	$4 \cdot 3 \pm 0 \cdot 5$	1.4 ± 0.0	$5 \cdot 1 \pm 1 \cdot 4$	$32 \cdot 4 \pm 6 \cdot 4$	18.6 ± 2.4	ND	$1 \cdot 6 \pm 0 \cdot 1$	42.8

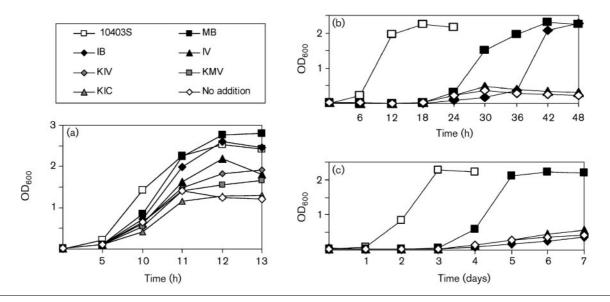


Fig. 4. Growth of *L. monocytogenes* strain *cld-2* in BHI with various supplements at 37 °C (a), 26 °C (b) and 10 °C (c). IV, IB and MB were added to a final concentration of 100 μM. KIC, KMV and KIV were added to a final concentration of 500 μM. *L. monocytogenes* 10403S was grown in BHI without supplement.

content was somewhat less than *cld-1*. IV showed less stimulatory activity than MB and IB. Supplementation of BHI medium with these precursors greatly increased the corresponding BCFAs. MB increased anteiso-C_{15:0} and anteiso-C_{17:0}, IB increased iso-C_{14:0} and iso-C_{16:0}, and IV increased iso-C_{15:0} and iso-C_{17:0} (Table 2), whereas the straight-chain fatty acid precursors propionate and butyrate increased the corresponding straight-chain fatty acid content (data not shown). In contrast, under the same conditions, these precursors did not show any significant effect on the fatty acid composition of wild-type 10403S

(data not shown). The overall total BCFA content was fully restored by MB and IB, and partially restored by IV, which was in accordance with the lower growth-stimulatory activity of IV compared to either MB or IB at 37 °C. IB greatly increased the even-numbered, iso-BCFAs in *cld-2* from 29 % to 88 %, and fully restored the growth. Moreover, increases of IV concentration further restored the odd-numbered, iso-BCFA content and growth (data not show). The IB- and IV-stimulated growth indicated that optimal growth at 37 °C could also be achieved by odd-numbered or even-numbered iso-BCFAs alone, without anteiso-BCFAs,

Table 2. Fatty acid composition of cld-2 in BHI with various supplements at 37 °C

The values are the means of at least two independent experiments \pm SEM; some minor fatty acid components are not shown. ND, Not detected.

Supplement*	Percentage (w/w) of total fatty acids									
	C _{14:0}	iso-C _{14:0}	C _{15:0}	Iso-C _{15:0}	Anteiso-C _{15:0}	C _{16:0}	Iso-C _{16:0}	Iso-C _{17:0}	Anteiso-C _{17:0}	BCFA
None	27.5 ± 0.7	13·6±1·6	5·2±0·6	1·0 ± 0·1	3·1 ± 0·3	30·8 ± 1·4	14·8 ± 1·5	ND	0·9±0·0	33.6
MB	1.7 ± 0.3	1.7 ± 0.6	1.2 ± 0.3	0.6 ± 0.1	48.4 ± 1.5	$7 \cdot 1 \pm 0 \cdot 7$	5·9 ± 1·7	ND	$33 \cdot 1 \pm 1 \cdot 9$	89.8
IB	$2 \cdot 4 \pm 0 \cdot 4$	40.2 ± 1.3	$1 \cdot 0 \pm 0 \cdot 3$	0.4 ± 0.1	$2 \cdot 0 \pm 0 \cdot 2$	4.9 ± 0.3	48.3 ± 0.6	ND	ND	91.2
IV	17.8 ± 5.3	17.4 ± 7.6	3.8 ± 0.3	13.6 ± 3.2	2.8 ± 0.5	$21 \cdot 6 \pm 5 \cdot 3$	18.5 ± 7.7	1.8 ± 0.3	0.7 ± 0.2	55.0
KMV	27.7 ± 0.9	7.5 ± 0.3	$4 \cdot 4 \pm 0 \cdot 2$	$1 \cdot 3 \pm 0 \cdot 1$	12.9 ± 0.5	$27 \cdot 2 \pm 0 \cdot 5$	10.6 ± 0.7	ND	3.8 ± 0.1	36.2
KIV	$22 \cdot 5 \pm 0 \cdot 2$	$23 \cdot 3 \pm 0 \cdot 3$	3.6 ± 0.1	$1\!\cdot\!1\pm0\!\cdot\!0$	$1 \cdot 7 \pm 0 \cdot 1$	20.5 ± 0.1	$24 \cdot 1 \pm 0 \cdot 5$	ND	0.4 ± 0.0	50.7
KIC	$28 \cdot 8 \pm 2 \cdot 3$	9.6 ± 1.6	5.5 ± 0.4	$6 \cdot 3 \pm 0 \cdot 3$	$2 \cdot 3 \pm 0 \cdot 3$	31.6 ± 1.5	10.5 ± 1.9	0.9 ± 0.1	0.6 ± 0.1	30.4
MB + IB	1.6 ± 0.1	29 ± 0.8	0.5 ± 0.0	0.3 ± 0.0	16.9 ± 2.4	$3 \cdot 0 \pm 0 \cdot 1$	$44 \cdot 4 \pm 2 \cdot 1$	ND	$4 \cdot 1 \pm 0 \cdot 6$	94.8
MB + IV	$1 \cdot 7 \pm 0 \cdot 2$	$3 \cdot 2 \pm 1 \cdot 2$	0.8 ± 0.2	22.9 ± 2.4	35.9 ± 1.0	5.0 ± 0.5	7.6 ± 2.7	5.6 ± 0.5	16.8 ± 0.8	92.2
Pyruvate	30.7 ± 0.4	10.2 ± 0.7	5.5 ± 0.1	$1 \cdot 4 \pm 0 \cdot 1$	$2 \cdot 6 \pm 0 \cdot 1$	$35 \cdot 4 \pm 1 \cdot 7$	11.7 ± 1.0	ND	0.7 ± 0.0	27.2

^{*}Supplements were added to the following final concentrations: MB, IB and IV, 100 μ M; KMV, KIV and KIC, 500 μ M; MB+IB, 50 μ M and 500 μ M, respectively; MB+IV, 50 μ M and 500 μ M, respectively; pyruvate, 500 μ M.

although anteiso-BCFAs are normally the most abundant BCFAs (>80%) in *L. monocytogenes* (Table 1).

Substrates of Bkd do not fully restore the growth of mutants

To further confirm that the Bkd complex in *cld-1* and *cld-2* was not functioning properly, the effect of KMV, KIV and KIC, which are all substrates of Bkd, was investigated. In contrast to the short BCFAs described above, these substrates, at concentrations of 100 µM, did not show any apparent stimulatory effect on growth (data not shown). At concentrations of 500 µM, KMV and KIV resulted in better growth of the mutants at 37 °C, whereas KIC only slightly stimulated growth (Fig. 4a). The corresponding BCFAs were also increased to some extent by these substrates (Table 2). However, the overall activities of substrates were significantly less than those of short BCFAs, and iso precursor KIV showed higher activity than KMV and KIC, which was not the case with short BCFAs, where anteiso precursor MB was most active (Fig. 1, Table 2). The low activities of Bkd substrates demonstrated that the Bkd in cld-1 and cld-2 was not functioning efficiently, or perhaps not at all.

Temperature affects the growth-stimulatory activities of the BCFA precursors

As described above, addition of short BCFAs extensively changed the fatty acid composition in bkd mutant cld-2 (Table 2). To clarify the influence of different fatty acid compositions on the growth of L. monocytogenes at low temperature, cld-2 was grown at different temperatures in medium supplemented with these BCFA precursors. The stimulatory activities of the short BCFAs showed significant temperature dependence. At 26 °C, MB and IB restored the growth of cld-2 to the same level as the wild-type, but there was a prolonged lag phase not observed with strain 10403S (Fig. 4b). IV exhibited no apparent growth-stimulatory activity at 26 °C. Only MB restored the growth of cld-2 at 10 °C (Fig. 4c). Furthermore, the temperature-dependent activity prompted us to examine whether IB and IV could depress the stimulatory activity of MB at low temperature. When IB, IV and MB were added at the same concentrations, IB and IV exhibited little or no effect (data not shown). However, an excess of IB and IV significantly depressed the growth-stimulatory activity of MB at 10 °C (Fig. 5). IB produced a stronger depression than IV, which was consistent with the fatty acid data showing that IB caused a greater decrease in anteiso-C_{15:0} (Table 2). In contrast, at 37 °C, the same excess of IB and IV did not depress the MB-stimulated growth, but stimulated growth to a level above that with MB alone (data not shown). These data demonstrate that although L. monocytogenes is able to achieve optimal growth at 37 °C when it has a high content of either anteiso-BCFAs or iso-BCFAs, there must be a substantial amount of anteiso-C_{15:0} for growth at low temperatures.

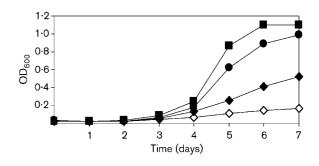


Fig. 5. Growth of *L. monocytogenes cld*-2 in BHI at 10 °C with mixed BCFA precursors. \diamondsuit , BHI without supplement; ■, 50 μ M MB; ●, 50 μ M MB plus 500 μ M IV; ♠, 50 μ M MB plus 500 μ M IB.

Pyruvate further decreases the BCFA content in cld-2

The decreased, but not completely abolished, BCFA content of the bkd mutants indicated that the ability to produce BCFA was not completely lost, and implied that a compensatory pathway was operating (Table 2). Subunits of Bkd and pyruvate dehydrogenase (PDH) in L. monocytogenes showed considerable homology (36–48% identity) (Glaser et al., 2001), and therefore PDH in cld-2 might metabolize branched-chain α -keto acids to short branched-chain acyl-CoA derivatives. This notion was supported by the observation that exogenous pyruvate further increased the straight-chain $C_{14:0}$ and $C_{16:0}$ fatty acids, and concomitantly decreased the BCFA content in cld-2 from 33% to 27% (Table 2). However, exogenous pyruvate did not affect the fatty acid composition of 10403S (data not shown).

bkd transcription is induced by substrates, but not low temperatures

The role of the Bkd substrates in the regulation of bkd expression was investigated by Northern analysis. As shown in Fig. 6, a 7 kb transcript was detected, which might cover the whole bkd cluster, suggesting that ptb, buk, lpd, bkdA1, bkdA2 and bkdB were co-transcribed as an operon. The 7 kb bkd transcript was induced by exogenous branched-chain α -keto acids (Fig. 6a), which was similar to bkd induction in B. subtils and E. faecalis (Debarbouille et al., 1999; Ward et al., 2000). Since cold-regulated BCFA synthesis is one of the major adaptive responses to low temperature, it was of interest to determine whether bkd expression was regulated by temperature. RNA isolated from strain 10403S grown at 37 °C and 10 °C was used to determine the role of low temperature in bkd transcription. As shown in Fig. 6(b), there was no significant difference between the bkd transcripts at 37 °C and 10 °C, indicating that the transcription of bkd remained at the same level when L. monocytogenes was grown at 37 °C and 10 °C.

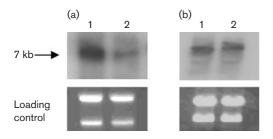


Fig. 6. Northern blot analysis of *bkd* transcription. (a) Total RNA was isolated from *L. monocytogenes* 10403S grown at 37 °C in BHI with the addition of 500 μM α -ketomethylvalerate (lane1), and without addition (lane 2). RNA (10 μg) was hybridized with a ³²P-labelled 1·4 kb DNA fragment spanning part of *buk* and *lpd.* (b) Total RNA was isolated from 10403S grown at 37 °C (lane 1) and 10 °C (lane 2). RNA (10 μg) was hybridized with a ³²P-labelled 0·4 kb fragment internal to *lpd* locus. The size of the band was determined by comparison with the RNA size marker. rRNA bands were used as a loading control (lower panel).

cld-2 retains its ability to adjust fatty acid composition in response to low temperature when provided with BCFA precursors

As described above, only the precursor for anteiso-BCFAs could restore the growth of bkd mutants at low temperature. This was consistent with the observation that the increase in anteiso- $C_{15:0}$ was the most significant fatty acid adaptation to $10\,^{\circ}$ C in strain 10403S (Table 3) (Annous *et al.*, 1997; Nichols *et al.*, 2002). In addition, the overall fatty acyl-chain length was shorter at $10\,^{\circ}$ C than at $37\,^{\circ}$ C (Table 3). These similar adjustments of fatty acid composition could be accomplished in cld-2, when the medium was supplemented with either MB or a mixture of MB, IB and IV. Specifically, anteiso- $C_{15:0}$ in cld-2 was greatly increased from $48\,\%$ to $70\,\%$ at $10\,^{\circ}$ C compared to $37\,^{\circ}$ C when the strain was grown in the presence of MB (Table 3).

Therefore, cld-2 retained the ability to increase the anteiso- $C_{15:0}$ content, and shorten the overall fatty acyl-chain length, when grown at low temperature, which were critical responses for cold adaptation. This implies that the Bkd is not the major cold-regulation point of fatty acid synthesis, and that this regulation probably occurs downstream of Bkd in the fatty acid synthesis pathway.

DISCUSSION

One reason that L. monocytogenes is a continuing food safety concern is its ability to grow at refrigeration temperatures. In this report, two Tn917-induced mutants showed deficiency in membrane BCFAs, and grew slowly at 37 °C and exceedingly slowly at low temperatures. DNA sequence homology suggested that Tn917 had inserted into the bkd cluster in the two strains. Genetic complementation and supplementation studies demonstrated that the Bkd in *L. monocytogenes* was responsible for the synthesis of branched-chain acyl-CoA derivatives, which are the starting units for BCFA biosynthesis. We also demonstrated the close correlation between membrane BCFA content, especially that of anteiso-C_{15:0}, and the growth ability of L. monocytogenes at optimal and low temperatures. Although functional Bkd is critical for growth at low temperatures, our data suggest that regulation of the Bkd is not the primary means of cold-regulation of BCFA biosynthesis in *L. monocytogenes*.

Since we sequenced the 5.6 kb bkd region of L. monocytogenes 10403S, the genome sequences of several L. monocytogenes strains have been published (Glaser et al., 2001; Nelson et al., 2004). The bkd regions in L. monocytogenes strains EGD-e and F2365 are composed of the genes lmo1369—lmo1374, and lmof2365_1386—lmof2365_1391, respectively. Genetic comparison of the bkd regions from the three L. monocytogenes strains showed synteny between the strains, with nearly complete identity at the DNA level. Northern blot analysis indicated that the six genes in this cluster (ptb,

Table 3. Fatty acid composition of *cld-2* in the presence of short BCFAs in BHI, and of 10403S in BHI, at 37 °C and 10 °C The values are the means of at least two independent experiments ±SEM; some minor fatty acid components are not shown. ND, Not detected; ECL, equivalent chain-length.

Strain	Temp.	Percentage (w/w) of total fatty acids											
		C _{14:0}	Iso C _{14:0}	C _{15:0}	Iso-C _{15:0}	Anteiso-15:0	C1 _{16:0}	Iso- _{16:0}	Iso- _{17:0}	Anteiso- _{17:0}	BCFA	ECL	
10403S	37	ND	0.7 ± 0.1	ND	10.4 ± 0.4	46.2 ± 0.6	0.9 ± 0.1	2.5 ± 0.1	3.4 ± 0.2	35.3 ± 0.4	98.7	15.7	
	10	ND	$1\!\cdot\!1\pm0\!\cdot\!1$	ND	12.6 ± 0.3	68.9 ± 1.2	ND	$1 \cdot 4 \pm 0 \cdot 1$	0.9 ± 0.1	14.3 ± 0.6	99.3	15.2	
cld-2	37*	1.7 ± 0.3	1.7 ± 0.6	$1\cdot 2\pm 0\cdot 3$	0.6 ± 0.1	48.4 ± 1.5	$7 \cdot 1 \pm 0 \cdot 7$	5.9 ± 1.7	ND	$33 \cdot 1 \pm 1 \cdot 9$	89.8	15.7	
	10*	3.8 ± 0.6	3.0 ± 0.6	0.6 ± 0.2	0.8 ± 0.1	70.5 ± 2.3	1.9 ± 0.2	3.7 ± 0.8	ND	13.8 ± 0.1	91.9	15.0	
cld-2	37†	1.4 ± 0.3	8.5 ± 1.8	0.6 ± 0.1	5.8 ± 0.6	$38 \cdot 0 \pm 2 \cdot 6$	$4 \cdot 3 \pm 0 \cdot 1$	$22 \cdot 6 \pm 2 \cdot 7$	$1 \cdot 3 \pm 0 \cdot 0$	17.4 ± 2.6	93.7	15.5	
	10†	$2 \cdot 3 \pm 0 \cdot 5$	16.3 ± 0.7	0.4 ± 0.0	$7 \cdot 1 \pm 0 \cdot 3$	$52 \cdot 7 \pm 2 \cdot 0$	$1 \cdot 0 \pm 0 \cdot 4$	11.9 ± 0.5	ND	6.2 ± 0.5	94.3	14.8	

^{*}Supplemented with 100 µM MB.

[†]Supplemented with a mixture of 100 μM MB, 100 μM IB and 100 μM IV.

buk, lpd, bkdA1, bkdA2 and bkdB) were co-transcribed, which was similar to what has been described for *Pseudomonas putida*, B. subtilis and E. faecalis (Burns et al., 1989; Debarbouille et al., 1999; Ward et al., 2000).

Homology searches also revealed that the Bkd in L. monocytogenes exhibited considerable homology to pyruvate dehydrogenase (PDH) from various bacteria (data not shown). PDH and Bkd were the only two members of the 2-keto acid dehydrogenase complex family in L. monocytogenes (Glaser et al., 2001) that catalysed the decarboxylation of 2-keto acids, and generated acyl-CoA derivatives. The Bkd mutations in L. monocytogenes were not lethal, whereas a B. subtilis strain with mutation in both Bkd and PDH required addition of BCFA precursors for growth (Willecke & Pardee, 1971). This suggests that PDH may compensate for the loss of Bkd activity to some extent. Indeed, in B. subtilis, PDH showed enzymic activity with branched-chain α-keto acids (Oku & Kaneda, 1988). The PDH enzymic preference (pyruvate > KIV > KMV > KIC) is perfectly consistent with the fatty acid profile in bkd mutants, where straight-chain and KIV-derived, evennumbered iso fatty acids rose to compensate for the decreased production of KMV- and KIC-derived oddnumbered fatty acids (Table 1). In addition, KIV was more efficient than KMV and KIC in stimulating growth, and restoring BCFA content (Table 2, Fig. 4). These observations did not match Bkd enzymic preference (KMV>KIV>KIC>pyruvate) (Oku & Kaneda, 1988). The further decrease in BCFA content to 27 % in mutant cld-2 via pyruvate was presumably because pyruvate competed with branched-chain α -keto acids for PDH. A level of 27 % BCFA might be close to the minimum BCFA necessary for growth of L. monocytogenes, in that further increases of pyruvate did not further decrease the BCFA in cld-2. Similarly, B. subtilis must have a minimum of 28 % BCFAs in the membrane in order to survive (Kaneda, 1991), and E. coli needs at least 20 % unsaturated fatty acids (Nunn et al., 1983).

Northern blot analysis showed that transcription of the bkd operon was not elevated by low temperature. This was consistent with the observation that total BCFA content was largely unchanged regardless of growth temperatures (Table 3). The major change in fatty acid composition was the increase of anteiso $C_{15:0}$ when L. monocytogenes was grown at low temperatures compared to 37 °C. The mechanism of cold-regulated synthesis of BCFAs remains elusive even in B. subtilis (de Mendoza et al., 2002; Lu et al., 2004). Strain cld-2 was able to accomplish a similar adjustment of fatty acid composition in response to low temperatures when BCFA precursors were provided. It seems that cold-regulated shortening of BCFA, in the presence of precursors, is not significantly impaired by the Bkd defect, indicating that Bkd is probably not the major cold-regulation point of fatty acid biosynthesis. Since incorporation of methyl-branches in BCFA could only be achieved by de novo biosynthesis of fatty acids (Suutari &

Laakso, 1994), the major cold-regulation point is likely to be located downstream of Bkd in the fatty acid biosynthesis pathway.

The substrate preferences of Bkd are involved in determining the ultimate cellular BCFAs, in that the precursor pool produced by Bkd is one major determinant in this pathway (Kaneda, 1991; Willecke & Pardee, 1971). The predominance of anteiso fatty acids in L. monocytogenes implies that, in this organism, Bkd has a higher affinity for isoleucine-derived substrates. Impaired Bkd could no longer preferentially produce anteiso precursors, and the fatty acid composition in cld-2 was largely dependent on the exogenous precursor pool (Table 3). Compared to 10403S (81%), the decreased total anteiso fatty acid content in cld-2 (55%) in the presence of a mixture of MB, IB and IV suggests that preference for anteiso precursors is partially lost due to the Bkd defect (Table 3). Therefore the role of Bkd in preferential synthesis of anteiso precursor may make Bkd essential for growth of L. monocytogenes at low temperatures.

The activities of MB, IB and IV in stimulating growth of Bkd mutants at 37 °C were also reported in B. subtilis and Myxococcus xanthus (Willecke & Pardee, 1971; Toal et al., 1995). Short BCFAs were activated to their acyl-CoA esters by acyl-CoA synthetase, and therefore compensated for the deficiency of BCFA precursors (Rock & Jackowski, 1985) (Fig. 1). Nevertheless, only the anteiso-BCFA precursor MB stimulated growth of Bkd mutants at 10 °C. The varying ability of BCFA precursors to support growth at different temperatures probably reflected the membrane fluidity requirements at that particular temperature. Although both iso-BCFAs and anteiso-BCFAs could provide sufficient membrane fluidity at 37 °C, only anteiso-C_{15:0} could provide the proper fluidity at low temperatures (Edgcomb et al., 2000; Jones et al., 2002). As a result, a substantial amount of anteiso-C_{15:0} was necessary for growth of L. monocytogenes at low temperatures. Supplementation with IB and IV led to increased iso-BCFAs at the expense of anteiso-BCFAs. The inhibitory activity of IB and IV on the growth of cld-2 in the presence of MB at low temperatures was probably due to competitive inhibition of enzymes in the fatty acid biosynthesis pathway, including the initiation enzyme FabH. Preference of these enzymes for isoleucine-derived substrates might explain why only large excesses of IB and IV showed activity. In conclusion, introduction of iso-BCFA-related metabolites should decrease anteiso-BCFA synthesis, and therefore depress or delay the growth at low temperature. This finding has the potential to be used to control the growth of L. monocytogenes, specifically at refrigeration temperatures.

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REFERENCES

- Annous, B. A., Becker, L. A., Bayles, D. O., Labeda, D. P. & Wilkinson, B. J. (1997). Critical role of anteiso-C_{15:0} fatty acid in the growth of *Listeria monocytogenes* at low temperatures. *Appl Environ Microbiol* 63, 3887–3894.
- Bayles, D. O., Annous, B. A. & Wilkinson, B. J. (1996). Cold-stress proteins induced in *Listeria monocytogenes* in response to temperature downshock and growth at low temperatures. *Appl Environ Microbiol* 62, 1116–1119.
- **Bryan, F. L. (2004).** The "danger zone" reevaluated. *Food Safety Mag* **10**, 55–69.
- **Burns, G., Brown, T., Hatter, K. & Sokatch, J. R. (1989).** Sequence analysis of the *lpdV* gene for lipoamide dehydrogenase of branched-chain-oxoacid dehydrogenase of *Pseudomonas putida. Eur J Biochem* **179,** 61–69.
- **Camilli, A., Portnoy, D. A. & Youngman, P. (1990).** Insertional mutagenesis of *Listeria monocytogenes* with a novel Tn*917* derivative that allows direct cloning of DNA flanking transposon insertions. *J Bacteriol* **172**, 3738–3744.
- **Choi, K., Heath, R. J. & Rock, C. O. (2000).** β -Ketoacyl-acyl carrier protein synthase III (FabH) is a determining factor in BCFA biosynthesis. *J Bacteriol* **182**, 365–370.
- **Debarbouille, M., Gardan, R., Arnaud, M. & Rapoport, G. (1999).** Role of BkdR, a transcriptional activator of the SigL-dependent isoleucine and valine degradation pathway in *Bacillus subtilis. J Bacteriol* **181**, 2059–2066.
- de Mendoza, D., Schujman, G. E. & Aguilar, P. S. (2002). Biosynthesis and function of membrane lipids. In *Bacillus subtilis and its Closest Relatives: from Genes to Cells*, pp. 43–55. Edited by A. L. Sonenshein, J. A. Hoch & R. Losick. Washington, DC: American Society for Microbiology.
- Edgcomb, M. R., Sirimanne, S., Wilkinson, B. J., Drouin, P. & Morse, R. P. D., II (2000). Electron paramagnetic resonance studies of the membrane fluidity of the foodborne pathogenic psychrotroph *Listeria monocytogenes. Biochim Biophys Acta* 1463, 31–42.
- Glaser, P., Frangeul, L., Buchrieser, C. & 53 other authors (2001). Comparative genomics of *Listeria* species. *Science* 294, 849–852.
- Jones, S. L., Drouin, P., Wilkinson, B. J. & Morse, P. D., II (2002). Correlation of long-range membrane order with temperature-dependent growth characteristics of parent and a cold-sensitive, branched-chain-fatty-acid-deficient mutant of *Listeria monocytogenes*. Arch Microbiol 177, 217–222.
- **Kaneda, T. (1991).** Iso- and anteiso-fatty acids in bacteria: biosynthesis, function, and taxonomic significance. *Microbiol Rev* **55**, 288–302.
- Lu, Y. J., Zhang, Y. M. & Rock, C. O. (2004). Product diversity and regulation of type II fatty acid synthases. *Biochem Cell Biol* 82, 145–155.
- Mead, P. S., Slutsker, L., Dietz, V., McCaig, F., Bresee, J. S., Shapiro, C., Griffin, P. M. & Tauxe, R. V. (1999). Food-related illness and death in the United States. *Emerg Infect Dis* 5, 607–625.

- Nelson, K. E., Fouts, D. E., Mongodin, E. F. & 30 other authors (2004). Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen *Listeria monocytogenes* reveal new insights into the core genome components of this species. *Nucleic Acids Res* 32, 2386–2395.
- Nichols, D. S., Presser, K. A., Olley, J., Ross, T. & McMeekin, T. A. (2002). Variation of branched-chain fatty acids marks the normal physiological range for growth in *Listeria monocytogenes*. Appl Environ Microbiol 68, 2809–2813.
- Nunn, W. D., Giffin, K., Clark, D. & Cronan, J. E., Jr (1983). Role for *fadR* in unsaturated fatty acid biosynthesis in *Escherichia coli*. *J Bacteriol* 154, 554–560.
- Oku, H. & Kaneda, T. (1988). Biosynthesis of branched-chain fatty acids in *Bacillus subtilis*. *J Biol Chem* 263, 18386–18396.
- Panoff, J., Thammavongs, B., Gueguen, M. & Boutibonnes, P. (1998). Cold-stress response in mesophilic bacteria. *Cryobiology* 36, 75–83.
- **Park, S. F. & Stewart, S. A. B. (1990).** High-efficiency transformation of *Listeria monocytogenes* by electroporation of penicillin-treated cells. *Gene* **94**, 129–132.
- Rock, C. O. & Jackowski, S. (1985). Pathway for the incorporation of exogenous fatty acids into phosphatidylethanolamine in *Escherichia coli. J Biol Chem* 260, 12720–12724.
- Sambrook, J., Fritsch, E. F. & Maniatis, T. (1989). *Molecular Cloning: a Laboratory Manual*, 2nd edn. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory.
- **Smith, K. & Youngman, P. (1992).** Use of a new integrational vector to investigate compartment-specific expression of the *Bacillus subtilis spoIIM* gene. *Biochimie* **74**, 705–711.
- Suutari, M. & Laakso, S. (1994). Microbial fatty acids and thermal adaptation. *Crit Rev Microbiol* 20, 285–328.
- **Toal, D. R., Clifton, S. W., Roe, B. A. & Downard, J. (1995).** The *esg* locus of *Myxococcus xanthus* encodes the E1a and E1b subunits of a branched chain keto acid dehydrogenase. *Mol Microbiol* **16**, 177–189.
- Wang, G., Kuriki, T., Roy, K. L. & Kaneda, T. (1993). The primary structure of branched-chain α -oxo acid dehydrogenase from *Bacillus subtilis* and its similarity to other α -oxo acid dehydrogenases. *Eur J Biochem* 213, 1091–1099.
- Ward, D. E., Ross, R. P., Weijden, C. C., Snoep, J. L. & Claiborne, A. (1999). Catabolism of branched-chain α -keto acids in *Enterococcus faecalis*: the *bkd* gene cluster, enzymes, and metabolic route. *J Bacteriol* 181, 5433–5441.
- Ward, D. E., Weijden, C. C., Merwe, M. J., Westerhoff, H. V., Claiborne, A. & Snoep, J. L. (2000). Branched-chain alpha-keto acid catabolism via the gene products of the *bkd* operon in *Enterococcus faecalis*: a new, secreted metabolite serving as a temporary redox sink. *J Bacteriol* 182, 3239–3246.
- **Weber, M. H. W. & Marahiel, M. A. (2002).** Coping with the cold: the cold-shock response in the Gram-positive soil bacterium *Bacillus subtilis. Philos Trans R Soc Lond B Biol Sci* **357**, 895–907.
- **Willecke, K. & Pardee, A. (1971).** Fatty acid-requiring mutant of *Bacillus subtilis* defective in branched chain α -keto acid dehydrogenase. *J Biol Chem* **246**, 5264–5272.